Evaluation of Genetic Structure Among Black Bears (*Ursus americanus*) in Kenai Fjords National Park and the Kenai Peninsula, Alaska

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Background

Black bears represent a significant component of the fjords ecosystem in southwest Alaska and are a focal attraction for visitors to Kenai Fjords N.P. (KEFJ). KEFJ park managers identified resource extraction, land development, landscape fragmentation, and hunting on the Kenai as immediate threats to the coastal ecosystem and resident wildlife including black bears. Black bears are highly mobile and apt to move over great distances. Genetic analyses offer important insights into the population structure and connectivity among such far-ranging animals. Genetic data provide information about historic and current levels of gene flow among populations, as well as information about genetic diversity, relatedness, and movement patterns within populations. Genetic information is essential to estimating population viability and evaluating possible management decisions. Mitochondrial DNA (mtDNA) sequence data provide important information about maternal gene flow patterns, past isolation events, natural recolonization events, and evolutionary history. Nuclear DNA (nDNA) microsatellites are highly variable markers that provide fine scale genetic resolution for identifying individuals, discerning close genetic relationships, and defining population units. Spatial patterns in genetic variation, or population structure, may arise due to various forms of isolation such as geographic distance, dispersal barriers, landscape resistance, and behavior or temporal factors.
(Moritz 1994, Waits 1999, Manel et al. 2003, Allendorf & Luikart 2007)

The objectives of this study included:

1. **Describe the phylogeographic relationship between black bears in south-central Alaska using mtDNA sequence data;**
2. **Determine the degree of genetic subdivision in the south-central Alaska black bear population;**
3. **Identify spatial patterns in genetic structure relative to the Kenai landscape.**

Genetic Methods

Sampling

- **Within KEFJ we used un-baited, non-invasive hair traps. Salmon streams and berry thickets provided a natural draw to hair traps which were set along bear trails.**
- **Across south-central Alaska, we supplemented our sampling with tissue samples from hunted bears.**

A black bear approaches a hair snare.
Photo courtesy of National Park Service

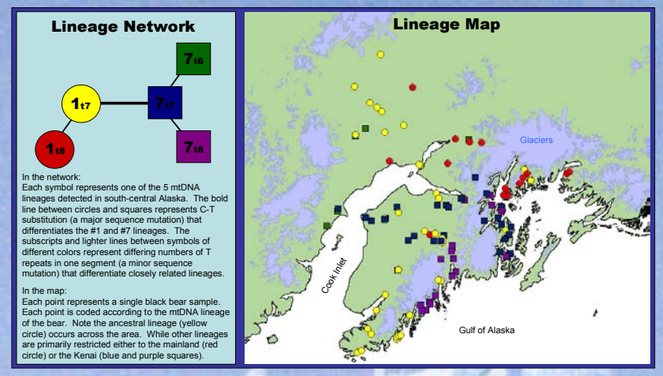
Laboratory

- **DNA was extracted from hair and tissue samples.**
- **The mtDNA control region was sequenced to analyze historic patterns of recolonization and isolation over a large geographic scale.**
- **13 Nuclear DNA microsatellites were genotyped to examine structure and gene flow at a fine spatial scale and the current generation.**

Analyses

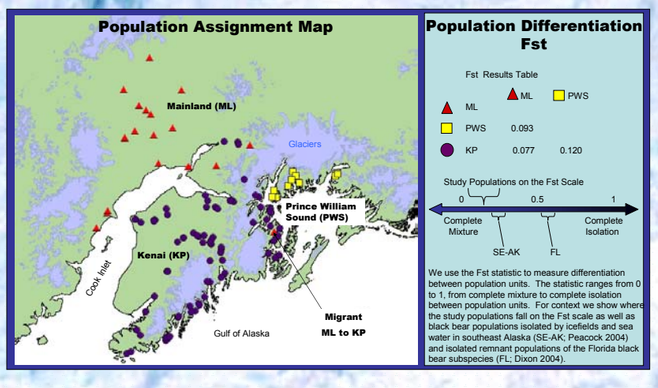
- **We constructed a network to show the evolutionary relationship between observed mtDNA lineages.**
- **We plotted mtDNA lineages on a map to examine their spatial relationships.**
- **With microsatellite genotypes we used Bayesian assignment tests to detect the most likely number of genetically distinct population units. (Corrander et al. 2006)**
- **We calculated Fst and the number of migrants between populations to quantify the degree of isolation between population units.**
- **We used local spatial autocorrelation to evaluate spatial patterns in genetic variation. (Anselin 1995, Sokal and Thomson 2006)**
- **We created a network of lines connecting neighboring points that shared a similar genetic make-up. This allowed us to visualize areas of higher and lower genetic connectivity.**

Phylogeography



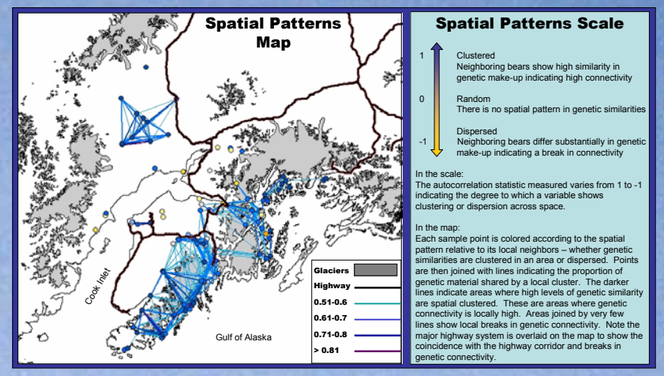
- **We detected 5 mtDNA lineages (a lineage = a unique mtDNA sequence).**
- **Lineages showed low divergence – or close evolutionary relationships (see network).**
- **There was a unique distribution of mtDNA lineages on the Kenai Peninsula and Alaskan mainland (see map).**
- **It is likely that black bears recolonized the area from a single continental refugium after the Pleistocene Ice Age.**
- **As ice sheets continued to melt and sea levels rose, the Kenai became increasingly cut off from the mainland. This isolated peninsular bear populations giving rise to distinct lineages on the Kenai.**

Population Structure



- **Assignment tests indicated 3 genetically distinct population units in the study area.**
- **Distinct units were identified on the Mainland (ML), Kenai Peninsula (KP), and Prince William Sound (PWS) (see map).**
- **Differentiation between groups was moderate as indicated by the relatively low Fst values between population units (see Fst table and scale).**
- **Some migration exists between population units; we detected one individual from the ML group on Kenai within the range of the KP group (see arrow on map).**
- **There was some overlap in group ranges where the KP met the ML (see map).**

Local Gene Flow



- **We detected spatial patterns in genetic variation indicating patchy genetic connectivity across the south-central Alaska study area.**
- **Major patches of genetic connectivity coincided with the three genetic population units identified by the assignment tests.**
- **Distinct patches of connectivity were apparent on the Kenai Peninsula.**
- **Patches of high connectivity coincided with breaks in eco-regions – from the Cook Inlet lowlands in the west to the Kenai Mountains in the east.**
- **Breaks in genetic connectivity also coincided with the major highways in the region.**
- **Dispersed points (those showing substantial genetic differences from near neighbors) occurred at the interfaces of genetic population units, and in the case of the ML-KP migrant identified in the assignment test.**

I&M Implications

- **Genetic distinction is evident between black bears on the Kenai Peninsula and other areas of south-central Alaska, indicating that bears on the Kenai are an important component of the genetic diversity of the species in the region.**
- **Genetic connectivity is currently high within the Kenai Peninsula, though it is not absolute.**
- **Maintaining current levels of connectivity will be important to preserving the genetic fitness and population viability of black bears on the Kenai Peninsula.**
- **Future investigations might focus on identifying dispersal corridors that maintain connectivity between genetic patches – particularly river valley systems.**
- **Local patches identified in the spatial analysis could serve as focal points for local management and future investigations of dispersal corridors.**
- **Genetic population units identified by assignment tests could serve as appropriate units for management on the regional scale.**

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For further information and details on analysis see:
Robinson SJ (2007) *Landscape Genetics of Black Bears (Ursus americanus) on the Kenai Peninsula, Alaska: Phylogenetic, Population Genetic and Spatial Analyses*. Master's Thesis, University of Idaho.
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